



Sequence Listing

<110> APROGEN INC.
<120> HUMANIZED ANTIBODY AND PROCESS FOR PREPARING SAME
<130> PCA30215/APG
<140> US/10/508,759
<141> 2004-09-22
<150> KR10-2002-0015708
<151> 2002-03-22
<160> 38
<170> KopatentIn 1.71
<210> 1
<211> 345
<212> DNA
<213> Artificial Sequence
<220>
<223> Variable region of humanized light chain HZVII
<400> 1
caggccgcggc tgggtcgatc tggagctgaa gtgaagaagc ctggggcctc agtgaaggtt 60
tcctgcaaaat cttctggcta cacccacc accgtgcttggaa tgaactgggt gcgacaggcc 120
cctggacagg gtcttgatg gatgggacgg atttatccta gtggtggaaat cactagctac 180
gcacagaagt tccagggcag agtcacaatg actgcagaca aatccacgag cacagtctac 240
atggagctca gcagcctgag atctgaggac acggcggtgtt attactgtgc aagagagttac 300
cgggtggccc gttggggcca aggaactctg gtcactgtct cttca 345

<210> 2
<211> 115
<212> PRT
<213> Artificial Sequence
<220>
<223> Variable region of humanized light chain HZVII
<400> 2
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ala Pro Gly Ala 15
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ala 20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45
Gly Arg Ile Tyr Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe 50 55 60
Gln Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Val Tyr 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Arg Val Ala Arg Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 3
<211> 336

<212> DNA

<213> Artificial Sequence

<220>
<223> variable region of humanized light chain HZIV

<400> 3
gatatcgtga tgacccaaac tccacttct ttgtcggtta cccctggaca accagcctct 60
atctcttgca agtcaagtca gagcctctta tatacgatgc gaaaaaccta tttgaattgg 120
ttattacaga agccaggcca gcctccacag cgccataatct atctgggtgc taatcggac 180
tctggagtcc ctgacaggtt cagttggcagt ggatcagggaa cagattttac actgaaaatc 240
agcagagtgg aggctgagga tggatggatc tattactgcg tgcaaggtac acatttcct 300
cagacgttcg gtggaggcac caaggtggaa atcaaa 336

<210> 4
<211> 112

<212> PRT

<213> Artificial Sequence

<220>
<223> variable region of humanized light chain HZIV

<400> 4
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly 15
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser 20 25 30
Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro 35 40 45
Pro Gln Arg Leu Ile Tyr Leu Val Ser Asn Arg Asp Ser Gly Val Pro 50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile 65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly 85 90 95
Thr His Phe Pro Gln Thr Phe Gly Gly Thr Lys Val Glu Ile Lys 100 105 110

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu94

<400> 5
gagaattcac attcacgatg tacttg 26

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR43-1

<400> 6
ctgctgcagc tggacctgac tctggacacc att 33

<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR44-1

<400> 7
caggcccaagc tgcagcagtc tggacctgaa ctg 33

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR45-1

<400> 8
tggcccttg gtggaggctg cagagacagt gac 33

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR46-1

<400> 9
gcctccacca agggcccatc ggtcttcccc ctg 33

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR31

<400> 10
cagcgccgc tcatttaccc gggacag 28

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu86

<400> 11
caaagcttgg aagcaagatg gattca 26

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR48

<400> 12
caagatatacc ccacaggtag cagatac 27

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR49

<400> 13
tgtggggata tcttgatgac ccaaact 27

<210> 14
<211> 27
<212> DNA
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<220>
<223> oligomer HUR50

<400> 14
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<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer HUR51

<400> 15
atcaaaagat ctgtggctgc accatct 27

<210> 16
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer CK1D

<400> 16
gccccgtcta gaattaacac tctccctgt tgaagcttt tgtgacggc gaactcag 58

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer YM001N

<400> 17
ccggaattca cattcacgt gtacttg 27

<210> 18
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer YM003

<400> 18
tgcccccaga ggtgct 16

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer ym257

<400> 19
acgcatttcag tgcttcttgg atgaactggg tga 33

<210> 20
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer YM258

<400> 20
atccaaagaag cactgaatgc gtagccagaa g 31

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer YM004

<400> 21
ccaattcaaaa gcgggttttc cattactata taagaggc 38

<210> 22
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer YM009

<400> 22
gcagccaccg tacgtttgat ttccacacctg gt 32

<210> 23
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu 166

<400> 23
ggatttgtct gcagtcatcg tggctctgcc ctggaaacctt 39

<210> 24
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Hur 37

<400> 24
gacaatcca cgagcacagt ctacatg 27

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu 118

<400> 25
ctgtggaggc tggcctggct tctgtataaa cca 33

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> oligomer Ryu 119

<400> 26
ggccagcctc cacagtcctt aatcttatctg 30

<210> 27
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized heavy chain KR127VH

<400> 27
caggtccagc tgcagcagtc tggacctgaa ctggtaagc ctggggcctc agtgaagatt 60
tcctgcaaag cttctggcta cgcatcagt agttcttggta tgaactgggt gaagcagagg 120
cctggacagg gtcttgagt gattggacgg atttacccctg gagatggaga tactaactac 180
aatggaaat tcaagggcaa ggccacactg actgcagaca aatccctccag cacagcctac 240
atgcagctca gcagcctgac ctctgtggac tctgcggctt atttctgtgc aagagagttac 300
gacgaggctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 28
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized heavy chain KR127VH

<400> 28
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Tyr Asp Glu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 29
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain KR127VK

<400> 29
gatatcttga tgacccaaac tccacttatt ttgtcggtta ccattggaca accagcctct 60
atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg
ttattacaga gcccaggcca gtctccaaag cgcctaattct atctgggtgc taaaactggac 120
tctggagtcc ctgacaggtt cactggcagt ggatcaggaa cagattttac actgaaaatc
atcagagtgg aggctgagga tttgggagtt tattactgcg tgcaaggtac acatttcct
cagacgttcg gtggaggcac caagctggaa atcaaa 180
300
336

<210> 30
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain KR127VK

<400> 30
Asp Ile Leu Met Thr Gln Thr Pro Leu Ile Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65	70	75	80
Ile Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Val Gln Gly			
85	90	95	
Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys			
100	105	110	

<210> 31
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> variable region of humanized heavy chain DP7

<400> 31
caggtgcagc tggtgccagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60
tcctgcagg catctggata cacccacc accactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatggaaata atcaacccta gtggtggtag cacaagctac 180
gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga 294

<210> 32
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> variable region of humanized heavy chain DP7

<400> 32
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr 20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45
Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe 50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr 65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95
Ala Arg

<211> 302
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain DPK12

<400> 33
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60
atctcctgca agtctagtca gagcctcctg catagtatg gaaagaccta tttgtattgg 120
tacctgcaga agccaggcca gcctccacag ctcctgatct atgaagttc caaccggttc 180
tctggagtgc cagataggtt cagttgcagc gggtcaggaa cagatttcac actgaaaatc 240
agccgggtgg aggctgagga tgttgggtt tattactgca tgcaaagtat acagcttcct 300
cc 302

<210> 34
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain DPK12

<400> 34
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30
Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45
Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95
Ile Gln Leu Pro
100

<210> 35
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized heavy chain HZ1

<400> 35
caggtccagc tgggtgcagtc tggagctgaa gtgggtgaagc ctggggcctc agtgaaggtt 60

tcctgcaaag cttctggcta cgcatcagt agttcttggta tgaactgggt ggcacaggcc 120
cctggacagg gtcttgaggta gattggacgg atttatcctg gagatggaga tactaactac 180
gcacagaagt tccagggcaa ggccacactg actgcagaca aatccacgag cacagcctac 240
atggagctca gcagcctgag atctgaggac acggcggtct atttctgtgc aagagagtac 300
gacgaggctt actggggcca aggaactctg gtcactgtct cttca 345

<210> 36
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable region of humanized heavy chain HZI

<400> 36
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala 1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser 20 25 30
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile 35 40 45
Gly Arg Ile Tyr Pro Gly Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe 50 55 60
Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr 65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys 85 90 95
Ala Arg Glu Tyr Asp Glu Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr 100 105 110
Val Ser Ser 115

<210> 37
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Variable region of humanized light chain HZI

<400> 37
gatatcttga tgacccaaac tccactttct ttgtcggtta cccctggaca accagcctct 60
atctcttgca agtcaagtca gagcctctta tatagtatg gaaaaaccta tttgaattgg 120
ttattacaga agccaggcca gtctccaaag cgcctaattct atctgggtgc taaaactggac 180
tctggagtcc ctgacaggtt cagtggcagt ggatcaggaa cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttggagtt tattactgcg tgcaaggatc acatttcct 300

cagacgttcg gtggaggcac caaggtggaa atcaaa

336

<210> 38
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> variable region of humanized light chain HZI

<400> 38
Asp Ile Leu Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30
Asn Gly Lys Thr Tyr Leu Tyr Trp Leu Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95
Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110